

1645  
RECEIVED

APR 19 2002

TECH CENTER 1600/2900

1600 Page 1 of 7

0590/0420



OIPE

ENTERED

RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

4 <110> APPLICANT: Huang, Qian  
5 Richmond, Joan F.L.  
6 Cho, Bryan K.  
7 Palliser, Deborah  
8 Chen, Jianzhu  
9 Eisen, Herman N.  
10 Young, Richard A.  
12 <120> TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
13 Protein Fusion Proteins Maps To A Discrete Domain and is  
14 CD4+T Cell-Independent  
17 <130> FILE REFERENCE: 0399.2006-003  
19 <140> CURRENT APPLICATION NUMBER: US 09/761,534A  
20 <141> CURRENT FILING DATE: 2001-01-16  
22 <150> PRIOR APPLICATION NUMBER: PCT/US00/32831  
23 <151> PRIOR FILING DATE: 2000-12-01  
25 <150> PRIOR APPLICATION NUMBER: US 60/176,143  
26 <151> PRIOR FILING DATE: 2000-01-14  
28 <160> NUMBER OF SEQ ID NOS: 25  
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
32 <210> SEQ ID NO: 1  
33 <211> LENGTH: 8  
34 <212> TYPE: PRT  
35 <213> ORGANISM: Unknown  
37 <220> FEATURE:  
38 <223> OTHER INFORMATION: Peptide Liberated From P1  
40 <400> SEQUENCE: 1  
41 Ser Ile Tyr Arg Tyr Tyr Gly Leu  
42 1 5  
45 <210> SEQ ID NO: 2  
46 <211> LENGTH: 8  
47 <212> TYPE: PRT  
48 <213> ORGANISM: Unknown  
50 <220> FEATURE:  
51 <223> OTHER INFORMATION: Ova Peptide  
53 <400> SEQUENCE: 2  
54 Ser Ile Ile Asn Phe Glu Lys Leu  
55 1 5  
58 <210> SEQ ID NO: 3  
59 <211> LENGTH: 8  
60 <212> TYPE: PRT  
61 <213> ORGANISM: Unknown  
63 <220> FEATURE:  
64 <223> OTHER INFORMATION: Alpha KG Peptide

## RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

```

66 <400> SEQUENCE: 3
67 Leu Ser Pro Phe Pro Phe Asp Leu
68 1 5
71 <210> SEQ ID NO: 4
72 <211> LENGTH: 5
73 <212> TYPE: PRT
74 <213> ORGANISM: Unknown
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Octapeptide
79 <400> SEQUENCE: 4
80 Ser Tyr Arg Gly Leu
81 1 5
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 1260
86 <212> TYPE: DNA
87 <213> ORGANISM: Unknown
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Mycobacterium Tuberculosis hsp70 cDNA
92 <220> FEATURE:
93 <221> NAME/KEY: CDS
94 <222> LOCATION: (1)...(1260)
98 <400> SEQUENCE: 5
99 atg gct cgt gcg gtc ggg atc gac ctc ggg acc acc aac tcc gtc gtc 48
100 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
101 1 5 10 15
103 tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc gag ggc 96
104 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
105 20 25 30
107 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
108 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
109 35 40 45
111 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
112 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
113 50 55 60
115 acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc ata gag 240
116 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
117 65 70 75 80
119 att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc att ctg 288
120 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
121 85 90 95
123 atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac att acc 336
124 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
125 100 105 110
127 gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag cgt cag 384
128 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
129 115 120 125
131 gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtg ctg cgg atc 432
132 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
133 130 135 140

```

## RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

135	gtc	aac	gag	ccg	acc	gcg	gcc	gcg	ctg	gcc	tac	ggc	ctc	gac	aag	ggc	480
136	Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Asp	Lys	Gly	
137	145					150					155					160	
139	gag	aag	gag	cag	cga	atc	ctg	gtc	ttc	gac	ttg	ggt	ggt	ggc	act	ttc	528
140	Glu	Lys	Glu	Gln	Arg	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	
141						165					170					175	
143	gac	gtt	tcc	ctg	ctg	gag	atc	ggc	gag	ggt	gtg	gtt	gag	gtc	cgt	gcc	576
144	Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Glu	Gly	Val	Val	Glu	Val	Arg	Ala	
145						180					185					190	
147	act	tcg	ggt	gac	aac	cac	ctc	ggc	ggc	gac	gac	tgg	gac	cag	cgg	gtc	624
148	Thr	Ser	Gly	Asp	Asn	His	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Val	
149						195										205	
151	gtc	gat	tgg	ctg	gtg	gac	aag	ttc	aag	ggc	acc	agc	ggc	atg	gat	ctg	672
152	Val	Asp	Trp	Leu	Val	Asp	Lys	Phe	Lys	Gly	Thr	Ser	Gly	Met	Asp	Leu	
153						210										220	
155	acc	aag	gac	aag	atg	gcg	atg	cag	cgg	ctg	cgg	gaa	gcc	gcc	gag	aag	720
156	Thr	Lys	Asp	Lys	Met	Ala	Met	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys	
157	225					230										240	
159	gca	aag	atc	gag	ctg	agt	tcg	agt	cag	tcc	acc	tcg	atc	aac	ctg	ccc	768
160	Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Leu	Pro	
161						245										255	
163	tac	atc	acc	gtc	gac	gcc	gac	aag	aac	ccg	ttg	ttc	tta	gac	gag	cag	816
164	Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Gln	
165						260										270	
167	ctg	acc	cgc	gcg	gag	ttc	caa	cgg	atc	act	cag	gac	ctg	ctg	gac	cgc	864
168	Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Asp	Arg	
169						275										285	
171	act	cgc	aag	ccg	ttc	cag	tcg	gtg	atc	gct	gac	acc	ggc	att	tcg	gtg	912
172	Thr	Arg	Lys	Pro	Phe	Gln	Ser	Val	Ile	Ala	Asp	Thr	Gly	Ile	Ser	Val	
173						290										300	
175	tcg	gag	atc	gat	cac	gtt	gtg	ctc	gtg	ggt	ggt	tcg	acc	cgg	atg	ccc	960
176	Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	
177	305					310										320	
179	gcg	gtg	acc	gat	ctg	gtc	aag	gaa	ctc	acc	ggc	ggc	aag	gaa	ccc	aac	1008
180	Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	Glu	Pro	Asn	
181						325										335	
183	aag	ggc	gtc	aac	ccc	gat	gag	gtt	gtc	gcg	gtg	gga	gcc	gct	ctg	cag	1056
184	Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln	
185						340										350	
187	gcc	ggc	gtc	ctc	aag	ggc	gag	gtg	aaa	gac	gtt	ctg	ctg	ctt	gat	gtt	1104
188	Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	
189						355										365	
191	acc	ccg	ctg	agc	ctg	ggt	atc	gag	acc	aag	ggc	ggg	gtg	atg	acc	agg	1152
192	Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Arg	
193						370										380	
195	ctc	atc	gag	cgc	aac	acc	acg	atc	ccc	acc	aag	cgg	tcg	gag	act	ttc	1200
196	Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	
197	385					390										400	
199	acc	acc	gcc	gac	gac	aac	caa	ccg	tcg	gtg	cag	atc	cag	gtc	tat	cag	1248

## RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

```

200 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
201                               405                               410                               415
203 ggg gag cgt gag
204 Gly Glu Arg Glu
205                               420
208 <210> SEQ ID NO: 6
209 <211> LENGTH: 420
210 <212> TYPE: PRT
211 <213> ORGANISM: Unknown
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Mycobacterium Tuberculosis hsp70 cDNA
217 <400> SEQUENCE: 6
218 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
219 1 5 10 15
220 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
221 20 25 30
222 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
223 35 40 45
224 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
225 50 55 60
226 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
227 65 70 75 80
228 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
229 85 90 95
230 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
231 100 105 110
232 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
233 115 120 125
234 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
235 130 135 140
236 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
237 145 150 155 160
238 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
239 165 170 175
240 Asp Val Ser Leu Leu Glu Ile Gly Glu Val Val Glu Val Arg Ala
241 180 185 190
242 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
243 195 200 205
244 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
245 210 215 220
246 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
247 225 230 235 240
248 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
249 245 250 255
250 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
251 260 265 270
252 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
253 275 280 285
254 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val

```

## RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

```

255      290      295      300
256 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
257 305      310      315      320
258 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
259      325      330      335
260 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
261      340      345      350
262 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
263      355      360      365
264 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
265      370      375      380
266 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
267 385      390      395      400
268 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
269      405      410      415
270 Gly Glu Arg Glu
271      420
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 630
276 <212> TYPE: DNA
277 <213> ORGANISM: Unknown
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Segment II of TBhsp70
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)...(630)
284 <223> OTHER INFORMATION: Segment II of TBhsp70
287 <400> SEQUENCE: 7
288 gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc act ttc 48
289 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
290 1 5 10 15
292 gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc 96
293 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
294 20 25 30
296 act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc 144
297 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
298 35 40 45
300 gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atg gat ctg 192
301 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
302 50 55 60
304 acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag 240
305 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
306 65 70 75 80
308 gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc 288
309 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
310 85 90 95
312 tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag 336
313 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
314 100 105 110
316 ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc 384

```

VERIFICATION SUMMARY

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:17

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw